

M. Wilson

1633

RAW SEQUENCE LISTING DATE: 05/04/2000
 PATENT APPLICATION: US/08/900,220B TIME: 13:10:49

Input Set : A:\ONV-044.01.txt
 Output Set: C:\CRF3\REFHOLD\05042000\H900220B.raw

ENTERED

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4 (1) GENERAL INFORMATION:
C--> 6 (i) APPLICANT: Miao, Ningning
7 Wang, Monica
8 Mahanthappa, Nagesh K.
9 Jin, Ping
10 Wang Pang, Kevin
12 (ii) TITLE OF INVENTION: Method of Treating Dopaminergic and
13 GABA-nergic Disorders
15 (iii) NUMBER OF SEQUENCES: 22
17 (iv) CORRESPONDENCE ADDRESS:
18 (A) ADDRESSEE: FOLEY, HOAG & ELIOT LLP
19 (B) STREET: ONE POST OFFICE SQUARE
20 (C) CITY: Boston
21 (D) STATE: MA
22 (E) COUNTRY: USA
23 (F) ZIP: 02109
25 (v) COMPUTER READABLE FORM:
26 (A) MEDIUM TYPE: Floppy disk
27 (B) COMPUTER: IBM PC compatible
28 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
29 (D) SOFTWARE: AscII (text)
C--> 31 (vi) CURRENT APPLICATION DATA:
C--> 32 (A) APPLICATION NUMBER: US/08/900,220B
C--> 33 (B) FILING DATE: 24-Jul-1997
34 (C) CLASSIFICATION:
36 (viii) ATTORNEY/AGENT INFORMATION:
37 (A) NAME: Vincent, Matthew P.
38 (B) REGISTRATION NUMBER: 36,709
39 (C) REFERENCE/DOCKET NUMBER: ONV-044.01
41 (ix) TELECOMMUNICATION INFORMATION:
42 (A) TELEPHONE: (617) 832-1000
43 (B) TELEFAX: (617) 832-7000
46 (2) INFORMATION FOR SEQ ID NO: 1:
47 (i) SEQUENCE CHARACTERISTICS:
48 (A) LENGTH: 1277 base pairs
49 (B) TYPE: nucleic acid
50 (C) STRANDEDNESS: both
51 (D) TOPOLOGY: linear
53 (ii) MOLECULE TYPE: cDNA
55 (ix) FEATURE:
56 (A) NAME/KEY: CDS
57 (B) LOCATION: 1..1275
59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
61 ATG GTC GAA ATG CTG CTG TTG ACA AGA ATT CTC TTG GTG GGC TTC ATC 48
62 Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile
63 1 5 10 15
65 TGC GCT CTT TTA GTC TCC TCT GGG CTG ACT TGT GGA CCA GGC AGG GGC 96

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 MAY 24 2000
 TC 1600 MAIL ROOM

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66 Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly
67          20          25          30
69 ATT GGA AAA AGG AGG CAC CCC AAA AAG CTG ACC CCG TTA GCC TAT AAG      144
70 Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
71          35          40          45
73 CAG TTT ATT CCC AAT GTG GCA GAG AAG ACC CTA GGG GCC AGT GGA AGA      192
74 Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg
75          50          55          60
77 TAT GAA GGG AAG ATC ACA AGA AAC TCC GAG AGA TTT AAA GAA CTA ACC      240
78 Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr
79          65          70          75          80
81 CCA AAT TAC AAC CCT GAC ATT ATT TTT AAG GAT GAA GAG AAC ACG GGA      288
82 Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly
83          85          90          95
85 GCT GAC AGA CTG ATG ACT CAG CGC TGC AAG GAC AAG CTG AAT GCC CTG      336
86 Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu
87          100          105          110
89 GCG ATC TCG GTG ATG AAC CAG TGG CCC GGG GTG AAG CTG CGG GTG ACC      384
90 Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr
91          115          120          125
93 GAG GGC TGG GAC GAG GAT GGC CAT CAC TCC GAG GAA TCG CTG CAC TAC      432
94 Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr
95          130          135          140
97 GAG GGT CGC GCC GTG GAC ATC ACC ACG TCG GAT CGG GAC CGC AGC AAG      480
98 Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys
99          145          150          155          160
101 TAC GGA ATG CTG GCC CGC CTC GCC GTC GAG GCC GGC TTC GAC TGG GTC      528
102 Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val
103          165          170          175
105 TAC TAC GAG TCC AAG GCG CAC ATC CAC TGC TCC GTC AAA GCA GAA AAC      576
106 Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn
107          180          185          190
109 TCA GTG GCA GCG AAA TCA GGA GGC TGC TTC CCT GGC TCA GCC ACA GTG      624
110 Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val
111          195          200          205
113 CAC CTG GAG CAT GGA GGC ACC AAG CTG GTG AAG GAC CTG AGC CCT GGG      672
114 His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly
115          210          215          220
117 GAC CGC GTG CTG GCT GCT GAC GCG GAC GGC CGG CTG CTC TAC AGT GAC      720
118 Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp
119          225          230          235          240
121 TTC CTC ACC TTC CTC GAC CGG ATG GAC AGC TCC CGA AAG CTC TTC TAC      768
122 Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr
123          245          250          255
125 GTC ATC GAG ACG CGG CAG CCC CGG GCC CTG CTA CTG ACG GCG GCC      816
126 Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Leu Thr Ala Ala
127          260          265          270
129 CAC CTG CTC TTT GTG GCC CCC CAG CAC AAC CAG TCG GAG GCC ACA GGG      864
130 His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly

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131          275          280          285
133 TCC ACC AGT GGC CAG GCG CTC TTC GCC AGC AAC GTG AAG CCT GGC CAA      912
134 Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln
135          290          295          300
137 CGT GTC TAT GTG CTG GGC GAG GGC GGG CAG CAG CTG CTG CCG GCG TCT      960
138 Arg Val Tyr Val Leu Gly Glu Gly Gly Gln Gln Leu Leu Pro Ala Ser
139 305          310          315          320
141 GTC CAC AGC GTC TCA TTG CGG GAG GAG GCG TCC GGA GCC TAC GCC CCA      1008
142 Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro
143          325          330          335
145 CTC ACC GCC CAG GGC ACC ATC CTC ATC AAC CGG GTG TTG GCC TCC TGC      1056
146 Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys
147          340          345          350
149 TAC GCC GTC ATC GAG GAG CAC AGT TGG GCC CAT TGG GCC TTC GCA CCA      1104
150 Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro
151          355          360          365
153 TTC CGC TTG GCT CAG GGC CTG CTG GCC GCC CTC TGC CCA GAT GGG GCC      1152
154 Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala
155          370          375          380
157 ATC CCT ACT GCC GCC ACC ACC ACT GGC ATC CAT TGG TAC TCA CGG      1200
158 Ile Pro Thr Ala Ala Thr Thr Thr Thr Gly Ile His Trp Tyr Ser Arg
159 385          390          395          400
160 CTC CTC TAC CGC ATC GGC AGC TGG GTG CTG GAT GGT GAC GCG CTG CAT      1248
161 Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His
162          405          410          415
164 CCG CTG GGC ATG GTG GCA CCG GCC AGC TG      1277
165 Pro Leu Gly Met Val Ala Pro Ala Ser
166          420          425
169 (2) INFORMATION FOR SEQ ID NO: 2:
171 (i) SEQUENCE CHARACTERISTICS:
172 (A) LENGTH: 1190 base pairs
173 (B) TYPE: nucleic acid
174 (C) STRANDEDNESS: both
175 (D) TOPOLOGY: linear
177 (ii) MOLECULE TYPE: cDNA
179 (ix) FEATURE:
180 (A) NAME/KEY: CDS
181 (B) LOCATION: 1..1191
183 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
185 ATG GCT CTG CCG GCC AGT CTG TTG CCC CTG TGC TGC TTG GCA CTC TTG      48
186 Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
187 1          5          10          15
189 GCA CTA TCT GCC CAG AGC TGC GGG CCG GGC CGA GGA CCG GTT GGC CGG      96
190 Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
191          20          25          30
193 CGG CGT TAT GTG CGC AAG CAA CTT GTG CCT CTG CTA TAC AAG CAG TTT      144
194 Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
195          35          40          45
197 GTG CCC AGT ATG CCC GAG CGG ACC CTG GGC GCG AGT GGG CCA GCG GAG      192

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198	Val	Pro	Ser	Met	Pro	Glu	Arg	Thr	Leu	Gly	Ala	Ser	Gly	Pro	Ala	Glu	
199		50					55					60					
201	GGG	AGG	GTA	ACA	AGG	GGG	TCG	GAG	CGC	TTC	CGG	GAC	CTC	GTA	CCC	AAC	240
202	Gly	Arg	Val	Thr	Arg	Gly	Ser	Glu	Arg	Phe	Arg	Asp	Leu	Val	Pro	Asn	
203	65					70				75						80	
205	TAC	AAC	CCC	GAC	ATA	ATC	TTC	AAG	GAT	GAG	GAG	AAC	AGC	GGC	GCA	GAC	288
206	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Ser	Gly	Ala	Asp	
207				85					90					95			
209	CGC	CTG	ATG	ACA	GAG	CGT	TGC	AAA	GAG	CGG	GTG	AAC	GCT	CTA	GCC	ATC	336
210	Arg	Leu	Met	Thr	Glu	Arg	Cys	Lys	Glu	Arg	Val	Asn	Ala	Leu	Ala	Ile	
211				100					105					110			
213	GCG	GTG	ATG	AAC	ATG	TGG	CCC	GGA	GTA	CGC	CTA	CGT	GTG	ACT	GAA	GGC	384
214	Ala	Val	Met	Asn	Met	Trp	Pro	Gly	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly	
215		115						120					125				
217	TGG	GAC	GAG	GAC	GGC	CAC	CAC	GCA	CAG	GAT	TCA	CTC	CAC	TAC	GAA	GGC	432
218	Trp	Asp	Glu	Asp	Gly	His	His	Ala	Gln	Asp	Ser	Leu	His	Tyr	Glu	Gly	
219		130					135					140					
221	CGT	GCC	TTG	GAC	ATC	ACC	ACG	TCT	GAC	CGT	GAC	CGT	AAT	AAG	TAT	GGT	480
222	Arg	Ala	Leu	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Arg	Arg	Asn	Lys	Tyr	Gly	
223	145					150				155						160	
225	TTG	TTG	GCG	CGC	CTA	GCT	GTG	GAA	GCC	GGA	TTC	GAC	TGG	GTC	TAC	TAC	528
226	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	
227				165					170					175			
229	GAG	TCC	CGC	AAC	CAC	ATC	CAC	GTA	TCG	GTC	AAA	GCT	GAT	AAC	TCA	CTG	576
230	Glu	Ser	Arg	Asn	His	Ile	His	Val	Ser	Val	Lys	Ala	Asp	Asn	Ser	Leu	
231				180					185					190			
233	GCG	GTC	CGA	GCC	GGA	GGC	TGC	TTT	CCG	GGA	AAT	GCC	ACG	GTG	CGC	TTG	624
234	Ala	Val	Arg	Ala	Gly	Gly	Cys	Phe	Pro	Gly	Asn	Ala	Thr	Val	Arg	Leu	
235		195						200					205				
237	CGG	AGC	GGC	GAA	CGG	AAG	GGG	CTG	AGG	GAA	CTA	CAT	CGT	GGT	GAC	TGG	672
238	Arg	Ser	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp	
239		210					215					220					
241	GTA	CTG	GCC	GCT	GAT	GCA	GCG	GGC	CGA	GTG	GTA	CCC	ACG	CCA	GTG	CTG	720
242	Val	Leu	Ala	Ala	Asp	Ala	Ala	Gly	Arg	Val	Val	Pro	Thr	Pro	Val	Leu	
243	225					230					235					240	
245	CTC	TTC	CTG	GAC	CGG	GAT	CTG	CAG	CGC	CGC	GCC	TCG	TTC	GTG	GCT	GTG	768
246	Leu	Phe	Leu	Asp	Arg	Asp	Leu	Gln	Arg	Arg	Ala	Ser	Phe	Val	Ala	Val	
247				245					250					255			
249	GAG	ACC	GAG	CGG	CCT	CCG	CGC	AAA	CTG	TTG	CTC	ACA	CCC	TGG	CAT	CTG	816
250	Glu	Thr	Glu	Arg	Pro	Pro	Arg	Lys	Leu	Leu	Leu	Thr	Pro	Trp	His	Leu	
251				260					265					270			
253	GTG	TTC	GCT	GCT	CGC	GGG	CCA	GCG	CCT	GCT	CCA	GGT	GAC	TTT	GCA	CCG	864
254	Val	Phe	Ala	Ala	Arg	Gly	Pro	Ala	Pro	Ala	Pro	Gly	Asp	Phe	Ala	Pro	
255		275						280					285				
257	GTG	TTC	GCG	CGC	CGC	TTA	CGT	GCT	GGC	GAC	TCG	GTG	CTG	GCT	CCC	GGC	912
258	Val	Phe	Ala	Arg	Arg	Leu	Arg	Ala	Gly	Asp	Ser	Val	Leu	Ala	Pro	Gly	
259		290						295				300					
261	GGG	GAC	GCG	CTC	CAG	CCG	CGC	CGC	GTA	GCC	CGC	GTG	GCG	CGC	GAG	GAA	960
262	Gly	Asp	Ala	Leu	Gln	Pro	Ala	Arg	Val	Ala	Arg	Val	Ala	Arg	Glu	Glu	

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Input Set : A:\ONV-044.01.txt

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```

263 305          310          315          320
265 GCC GTG GGC GTG TTC GCA CCG CTC ACT GCG CAC GGG ACG CTG CTG GTC      1008
266 Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
267          325          330          335
269 AAC GAC GTC CTC GCC TCC TGC TAC GCG GTT CTA GAG AGT CAC CAG TGG      1056
270 Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
271          340          345          350
273 GCC CAC CGC GCC TTC GCC CCT TTG CGG CTG CTG CAC GCG CTC GGG GCT      1104
274 Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
275          355          360          365
277 CTG CTC CCT GGG GGT GCA GTC CAG CCG ACT GGC ATG CAT TGG TAC TCT      1152
278 Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
279          370          375          380
281 CGC CTC CTT TAC CGC TTG GCC GAG GAG TTA ATG GGC TG      1190
282 Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly
283 385          390          395
286 (2) INFORMATION FOR SEQ ID NO: 3:
288 (i) SEQUENCE CHARACTERISTICS:
289 (A) LENGTH: 1281 base pairs
290 (B) TYPE: nucleic acid
291 (C) STRANDEDNESS: both
292 (D) TOPOLOGY: linear
294 (ii) MOLECULE TYPE: cDNA
297 (ix) FEATURE:
298 (A) NAME/KEY: CDS
299 (B) LOCATION: 1..1233
301 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
303 ATG TCT CCC GCC TGG CTC CGG CCC CGA CTG CGG TTC TGT CTG TTC CTG      48
304 Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu
305 1          5          10          15
307 CTG CTG CTG CTT CTG GTG CCG GCG GCG CGG GGC TGC GGG CCG GGC CGG      96
308 Leu Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg
309          20          25          30
311 GTG GTG GGC AGC CGC CGG AGG CCG CCT CGC AAG CTC GTG CCT CTT GCC      144
312 Val Val Gly Ser Arg Arg Arg Pro Arg Lys Leu Val Pro Leu Ala
313          35          40          45
315 TAC AAG CAG TTC AGC CCC AAC GTG CCG GAG AAG ACC CTG GGC GCC AGC      192
316 Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
317          50          55          60
319 GGG CGC TAC GAA GGC AAG ATC GCG CGC AGC TCT GAG CGC TTC AAA GAG      240
320 Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
321 65          70          75          80
323 CTC ACC CCC AAC TAC AAT CCC GAC ATC ATC TTC AAG GAC GAG GAG AAC      288
324 Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
325          85          90          95
327 ACG GGT GCC GAC CGC CTC ATG ACC CAG CGC TGC AAG GAC CGT CTG AAC      336
328 Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
329          100          105          110
331 TCA CTG GCC ATC TCT GTC ATG AAC CAG TGG CCT GGT GTG AAA CTG CGG      384

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VERIFICATION SUMMARY

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TIME: 13:10:50

Input Set : A:\ONV-044.01.txt

Output Set: C:\CRF3\REFHOLD\05042000\H900220B.raw

L:6 M:220 C: Keyword misspelled, [(i) APPLICANT:]
L:792 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:1734 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2258 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2264 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2291 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2294 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2298 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2321 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2327 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2330 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2333 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2336 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2339 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2342 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2345 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22